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(54) Title: METHOD AND MEANS FOR PRODUCING A PROTEIN HAVING THE SAME IgG SPECIFICITY AS PROTEIN G

	ACT	TAC	AAA	TTA	ATC	CTT	AAT	GGT	AAA	ACA	TTG	AAA	GGC	GAA	ACA	ACT
C1	Thr	Tyr	Lys	Leu	Ile	Leu	Asn	Gly	Lys	Thr	Leu	Lys	Gly	Glu	Thr	Thr
C2	-	-	-	-	Val	Ile	-	-	-	-	-	-	-	-	-	-
C3	-	-	-	-	Val	Ile	-	-	-	-	-	-	-	-	-	-

	ACT	GAA	GCT	GTT	GAT	GCT	GCT	ACT	GCA	GAA	AAA	GTC	TTC	AAA	CAA	TAC
C1	Thr	Glu	Ala	Val	Asp	Ala	Ala	Thr	Ala	Glu	Lys	Val	Phe	Lys	Gln	Tyr
C2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C3	-	Lys	-	-	-	-	Glu	-	-	-	-	Ala	-	-	-	-

	GCT	AAC	GAC	AAC	GGT	GTT	GAC	GGT	GAA	TGG	ACT	TAC	GAC	GAT	GCG	ACT
C1	Ala	Asn	Asp	Asn	Gly	Val	Asp	Gly	Glu	Trp	Thr	Tyr	Asp	Asp	Ala	Thr
C2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C3	-	-	-	-	-	-	-	-	Val	-	-	-	-	-	-	-

	AAG	ACC	TTT	ACA	GTT	ACT	GAA		AAA	CCA	GAA	GTG	ATC	GAT	GCG
C1	Lys	Thr	Phe	Thr	Val	Thr	Glu	D1	Lys	Pro	Glu	Val	Ile	Asp	Ala
C2	-	-	-	-	-	-	-	D2	-	-	-	-	-	-	-
C3	-	-	-	-	-	-	-								

	TCT	GAA	TTA	ACA	CCA	GCC	GTG	ACA
D1	Ser	Glu	Leu	Thr	Pro	Ala	Val	Thr
D2	-	-	-	-	-	-	-	-

(57) Abstract

Method for producing a protein having the same IgG specificity as protein G from group G Streptococci, strain G148. The invention also relates to a recombinant DNA molecule coding for said protein, and to microorganisms containing this recombinant DNA molecule.

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Method and means for producing a protein having
the same IgG specificity as protein G

The invention relates to the field of gene technology and is concerned with recombinant DNA molecules, which contain a nucleotide sequence coding for a protein or polypeptide of the same IgG specificity as protein G from group G Streptococci strain G148. Moreover the invention comprises microorganisms containing the aforesaid molecules, and the use thereof in the production of the aforesaid protein or polypeptide.

The existence of bacterially produced proteins or polypeptides binding selectively to the Fc portion of immunoglobulins has been known for decades. Among such proteins the one that has been investigated most thoroughly is protein A from *Staphylococcus aureus*; and this is actually the only protein of that group which has acquired commercial importance (Protein A and Protein A Sepharose[®] from Pharmacia AB, Uppsala, Sweden). Sjöquist (FEBS Letters 28(1) (1972) p. 73-76 and US patents 3,850,798 and 3,995,018) made the discovery that one component of the protein A-IgG system when immobilized on an insoluble polymer could be employed for binding the other component, and it became thus possible to purify the protein on a large scale and, also, to develop a very simple and selective method for the isolation of antibodies. The specificity of the protein for various different immunoglobulins has been studied in great detail; see for instance Forsgren, A. et al., *Staphylococci and Staphylococcal Infections* 2 (1983), p. 429-479, Academic Press Inc. (London). A remarkable feature of that protein is its low affinity for the IgG subclass IgG₃ of the human system. In view of the fact that this subclass amounts to about 8 % of the total IgG content in serum supplementary

purification steps are required for isolating all classes of IgG.

However, already in 1973 Kronvall (J. Immunol. 111(5) (1973) p. 1401-6) showed that also group C and G Streptococci carry components on their surface which have affinity for IgG. The experiments furthermore showed that their reactivity in this respect was a non-immunoreactivity, that is, the immunoglobulin was not bound via its antigen combining sites in the Fab portions, and the results indicated that IgG₃ too was bound in this system. This Fc-binding component has later on been found to be of a protein nature and has been given the name of "protein G". Therefore, as a supplement to the Staphylococcus aureus protein A or as a total or partial replacement thereof, protein G would be a natural choice among bacterially produced proteins capable of binding to the Fc portion of IgG class immunoglobulins, for example for the purpose of purifying IgG (US 3,995,018). But the protein has not been studied to any major extent, due to problems involved with its liberation from the bacterium.

In Journal of Immunol. 133(2) p. 969 Björck and Kronvall in 1984 published a method by which small amounts of the protein were set free from the bacterium by means of enzymatic degradation with papain. This method will give a material enabling limited functional and structural studies to be carried out, but the yields are far too low for commercial use, e.g. for the purification of monoclonal antibodies. Quite generally also it may be difficult to obtain a homogeneous and reproducible product with such a method. Moreover Streptococci are pathogenic and necessitate the use of complex culturing media which involve complications in large-scale cultures. There is thus a need for a new method of producing Fc-binding proteins or fragments thereof from Streptococci of types C and G.

The present invention relates to a recombinant DNA molecule comprising a nucleotide sequence which codes for a protein

or polypeptide having the same IgG specificity as protein G from group G Streptococci strain G148. The natural source of this nucleotide sequence is of course the said bacterial strain, but quite conceivably also recourse may be had to synthetically produced molecules, in particular for the active polypeptides. The term "active polypeptides" in this context refers to polypeptides that have the aforesaid IgG specificity.

For producing a recombinant DNA molecule according to the invention a suitable cloning vehicle or vector, for example a plasmid or phage DNA, may be cleaved with the aid of a restriction enzyme whereupon the DNA sequence coding for the desired protein or polypeptide is inserted into the cleavage site to thus form the recombinant DNA molecule. This general procedure is known per se, and various techniques for cleaving and ligating DNA sequences have been described in the literature (see for instance US 4,237,224); but to the best of our knowledge these techniques have not been used in the present protein system. If the bacterial strain Streptococcus G148 is employed as the source of the desired nucleotide sequence it is possible to isolate said sequence and to introduce it into a suitable vector in a manner such as described in the experimental part below.

Hosts that may be employed - that is, microorganisms which are caused to produce the protein or active fragments thereof - may comprise bacterial hosts such as strains of e.g. Escherichia, Bacillus, Streptococcus, Staphylococcus and furthermore yeasts and other eukaryotic cells in culture. Among bacterial hosts those of the gram-positive type are preferred because of the fact that their cell wall contains only one membrane system. If the protein or the active fragment is produced in combination with a signal peptide suiting the system then the product is directly secreted into the medium. Numerous signal peptides have been published during recent years, see for example WO 84/00774; to persons skilled in the art it is a matter of well-known

routine to choose and employ signal peptides apt to give a good secretion in various bacterial systems. For obtaining maximum expression, regulatory elements such as promoters and ribosome-binding sequences may be varied in a manner known per se.

The invention thus comprises recombinant DNA molecules containing a nucleotide sequence which codes for a protein or polypeptide having the same IgG specificity as protein G from *Streptococcus* G148. As will be seen from the experimental portion of this specification the protein G gene has the following nucleotide sequences C1, C2 and C3 coding for IgG-binding polypeptides:

C1

ACT TAC AAA TTA ATC CTT AAT GGT AAA ACA TTG AAA GGC GAA ACA
ACT ACT GAA GCT GTT GAT GCT GCT ACT GCA GAA AAA GTC TTC AAA
CAA TAC GCT AAC GAC AAC GGT GTT GAC GGT GAA TGG ACT TAC GAC
GAT GCG ACT AAG ACC TTT ACA GTT ACT GAA

C2

ACT TAC AAA CTT GTT ATT AAT GGT AAA ACA TTG AAA GGC GAA ACA
ACT ACT GAA GCT GTT GAT GCT GCT ACT GCA GAA AAA GTC TTC AAA
CAA TAC GCT AAC GAC AAC GGT GTT GAC GGT GAA TGG ACT TAC GAC
GAT GCG ACT AAG ACC TTT ACA GTT ACT GAA

and C3

ACT TAC AAA CTT GTT ATT AAT GGT AAA ACA TTG AAA GGC GAA ACA
ACT ACT AAA GCA GTA GAC GCA GAA ACT GCA GAA AAA GCC TTC AAA
CAA TAC GCT AAC GAC AAC GGT GTT GAT GGT GTT TGG ACT TAT GAT
GAT GCG ACT AAG ACC TTT ACG GTA ACT GAA

The invention thus relates to recombinant DNA molecules which contain one or more of the said nucleotide sequences or analogous sequences. The term "analogous sequences" means

sequences coding for polypeptides of the aforesaid IgG specificity.

Furthermore the invention comprises vectors such as e.g. plasmids and phages containing such a nucleotide sequence, and microorganisms, especially bacteria as e.g. strains of *Escherichia*, *Bacillus* and *Staphylococcus*, into which such a vector has been introduced. Alternatively, such a nucleotide sequence may be integrated into the natural gene material of the microorganism.

The application furthermore relates to a method for the production of a protein or polypeptide having the same IgG specificity as protein G from *Streptococcus* G148. According to this method, a microorganism as set forth above is cultured in a suitable medium whereupon the resultant product is isolated by affinity chromatographic purification with the aid of IgG bound to an insoluble carrier, or by means of some other separating method, for example ion exchange chromatography.

Vectors, especially plasmids, which contain the protein G-encoding nucleotide sequence may advantageously be provided with a readily cleavable restriction site by means of which a nucleotide sequence that codes for another product can be fused to the protein G-encoding nucleotide sequence, to thus express a so-called fusion protein. The fusion protein may be isolated by a procedure utilizing its capacity of binding to IgG, whereupon the other component of the system may if desired be liberated from the fusion protein. This technique has been described at length in WO 84/03103 in respect of the protein A system and is applicable also in the present context in an analogous manner. Since protein G and protein A have binding properties partially complementary to each other a fusion protein containing both of these components is a potentially attractive product.

In one aspect of the invention a nucleotide sequence as defined above is fused to a gene sequence coding for protein A or an active fragment thereof in a fusion vector and accordingly in one molecule coding for a fusion protein with combined protein A and protein G binding characteristics. Vectors and microorganisms as defined above but containing this specific nucleotide sequence is another aspect of the invention. A further aspect is the fusion protein or polypeptide having the combined protein A and protein G binding characteristics, encoded by said nucleotide sequence or produced in an equivalent way.

Starting materials and general procedures

Streptococcus G148 which is a human group G strain was obtained from Statens Veterinärmedicinska Anstalt (SVA), Uppsala, Sweden.

E. coli strains HB101 (Boyer, HW and Roulland-Dussoix, D, J. Mol. Biol. 41(1969) p. 459-472 and JM 105 (Messing, J. and Carlsson, J., J. Biotechnol. 1(1984) p. 253-264 were employed as bacterial hosts for the plasmids to be constructed; and the strains NM538 and NM539 were used in cloning with the lambda vector EMBL3a (Frischauf, A-M et al., J. Mol. Biol. 170(1983) p. 827-842. The plasmid vectors employed were pUC13, pUC18, and pUC19 (Norrande, J. et al., Gene 26(1983), p. 101-106), and pBR322 (Bolivar, F et al. Gene 2 (1977) p. 95-113.

Culture media

The medium set forth below is employed for culturing E. coli bacteria. Amounts as stated are per 1 liter of medium.

Trypton Soy Broth (Oxoid Ltd Basingstoke, Hants., England)	30	g
Yeast Extract (Oxoid)	10	g
D-glucose	40	g
NH ₄ Cl	2.5	g
Na ₂ HPO ₄ ·2H ₂ O	7.5	g
KH ₂ PO ₄	3.0	g
Na ₂ SO ₄ ·10H ₂ O	2.5	g
MgSO ₄ ·7H ₂ O	0.2	g
CaCl ₂ ·2H ₂ O	0.5	mg
FeCl ₃ ·6H ₂ O	16.7	mg
ZnSO ₄ ·7H ₂ O	0.18	mg
CuSO ₄ ·5H ₂ O	0.16	mg
MnSO ₄ ·4H ₂ O	0.15	mg
CoCl ₂	0.10	mg
NaEDTA	20.1	mg

The medium set forth below is employed for culturing Streptococcus G148. Here again, the amounts refer to the contents per 1 liter of culture medium.

Yeast Extract (Oxoid)	50	g
Trypton Soy Broth (Oxoid)	30	g
L-alanine	0.69	g
L-asparagine	0.30	g
L-arginine	0.50	g
L-glutamine	0.43	g
glycine	0.28	g
L-histidine	0.15	g
L-isoleucine	0.22	g
L-leucine	0.33	g
L-lysine	0.27	g
L-methionine	0.09	g
L-phenylalanine	0.35	g
L-proline	0.50	g
L-serine	0.26	g

L-threonine	0.20 g
L-tryptophan	0.07 g
L-tyrosine	0.03 g
L-valine	0.26 g

DNA preparations

Streptococcus G148 cells were cultured in Todd-Hewitt medium (Oxoid Ltd Basingstoke, Hants., England). The cells were washed and then resuspended in a cell-free medium from Streptomyces griseus 9179 (1/20 of the original volume), whereupon lysozyme was added to a concentration of 1 mg/ml. The Streptomyces strain which had been obtained from Dr. W. Köhler, Institute für Mikrobiologie und experimentelle Therapie, Jena, DDR) had been cultured in the manner as described by Prauser and Köhler in Zeitschrift für allg. Mikrobiologie vol. 5(4) (1965) p. 308-314 for inducing lytic activity. When the Streptococcus cells had been incubated in the medium for 2 hours at 37 °C the DNA was extracted as described by Marmur, J, J. Mol. Biol. 3(1961) p. 208-218.

Plasmid DNA from E. coli was prepared by alkaline extraction (Birnboim, HC et al. Nucleic Acids Res. 7(1979) p. 1513-1523).

Lambda DNA was prepared as described by Maniatis et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York 1982).

Plasmid transformations were performed as described by Morrison et al. (Methods Enzymol. 68(1979) p. 326-331).

Restriction endonucleases, T4 DNA ligase, DNA polymerase I and Klenow fragments were obtained from New England Biolabs (Boston, USA) or from Boehringer Mannheim (Mannheim, Federal Republic of Germany) and were employed in conformity with the manufacturers' directions.

Example 1. Isolation of a lambda clone which codes for polypeptides possessing IgG-binding activity

A gene library for Streptococcus G148 was produced in a manner analogous to that described by Frischauf et al. (1983, see above).

Streptococcal DNA was partially digested with Sau3A and ligated into BamHI-cleaved lambda vector EMBL3a. The ligated DNA was packaged in vitro into phage particles which were then allowed to infect E. coli NM539 cells. The resultant phage library was analyzed for IgG-binding activity, the phages being titrated for this purpose on agar plates which were incubated overnight at 37 °C. The next day plates having a plaque frequency of $10^3 - 10^4$ were selected. A nitrocellulose filter (Schleicher & Schüll, Membranefilter BA85 (0.45 micrometer) Dassel, Federal Republic of Germany) was placed onto each of these selected plates. Blotting was allowed to proceed at room temperature for about 10 minutes. whereupon the filters were immersed for 1 hour in phosphate-buffered sodium chloride solution (PBS) containing Tween 20 to 0.1 % concentration. The filter papers were then transferred to a petri dish containing approximately 10^7 cpm of ^{125}I -labeled rabbit-IgG-antibodies (specific activity 7 mCi/mg) in PBS with an addition of 0.05 % Tween 20 (PBST). After a 2-hour period of incubation at room temperature the filter papers were washed twice for 10 minutes in PBST and then dried. Autoradiographic analysis of the filter papers indicated the positive lambda clones which produced polypeptides binding the radioactive antibodies. These clones were selected on the original agar plate and analyzed again. Finally a clone called "lambda SPG1" was chosen for the subsequent procedures. A further possibility, in addition to using the above-enumerated systems, will of course be to propagate lambda SPG1 in suitable strains of E. coli for producing the desired protein.

Example 2. DNA sequencing

The EMBL3a lambda vector has a structure such that DNA fragments ligated into BamHI sites are flanked on both sides by SalI sites. Cleavage of lambda SPG1 DNA with SalI gave two fragments of about 2.1 kilobase pairs (kb) and 12 kb respectively, deriving from the Streptococcal DNA fragment that had been inserted originally. These two fragments were ligated into SalI-cleaved pUC19 to thus produce the two recombinant plasmids pSPG1 and pSPG8 containing 2.1 kb and 12 kb fragments respectively. Transformants of *E. coli* HB101 containing the said respective plasmids were cultured in Luria broth (Maniatis et al.) with addition of ampicillin to a final concentration of 50 micrograms/ml, whereupon the cell lysate (Löfdahl et al., Proc. Natl. Acad. Sci. USA 80 (1983), p. 697-701) was tested for IgG-binding activity. This was done by means of the hemagglutination test (Guss et al., Eur. J. Biochem. 153 (1985) p. 579-585). An *E. coli* clone containing the plasmid pSPG1 was positive in this test.

The plasmid pSPG1 which contained an IgG binding portion of the protein G gene from *Streptococcus* G148 was digested with appropriate restriction enzymes; DNA fragments thus formed were cloned into the replicative form of the phage M13 and were then transformed into *E. coli* strain JM105. The nucleotide sequence of the inserted DNA fragments was analyzed by means of the so-called dideoxy method (Sanger F., Nicklen, S. and Coulson, AR (1977), Proc. Natl. Acad. Sci. USA 74, 5463-5467).

Fig. 1(a) shows the restriction map of pSPG1. A 1.5 kb EcoRI/HindIII fragment covering the range from 0.28 to 1.73 kb in Fig. 1(a) was cloned into pUC18 and pUC19 to thus give pSPG2 and pSPG3 respectively. The complete sequence of these is shown in Fig. 2. The regions that can be located in this sequence are set forth in Fig. 1(b) showing repetitive

structures A1, A2 and A3 coding for 24 amino acids each and interrupted by sequences B1 and B2 (51 amino acids) which too are repetitive. A so-called spacer region S is followed by repetitive regions C1, C2 and C3 corresponding to 55 amino acids each and interrupted by regions D1 and D2 (15 amino acids). Next follows a hydrophilic portion, W, which has a structure similar to that of the so-called X_r region of the protein A system (Guss et al. (1984) Eur. J. Biochem. 138, p. 413-420).

Results obtained from amino acid analysis of the products from pSPG1, pSPG2 and pSPG3 (Fig. 1c) when compared with the protein A system indicated that both the W and the M regions are involved in cell wall - cell membrane interaction. The other regions could be subjected to a closer study with the aid of a number of subclones, pSPG4 - pSPG7 (Fig. 1 c). In that Figure, sequences coding for an IgG-binding product are indicated by means of a "+" sign, the rest being indicated by a "-" sign. It was found that pSPG4 and pSPG7 coded for non-binding products; so the part of the sequence expressing binding polypeptides is located in the C regions, that is, C1, C2 and C3.

Fig. 3 compares the homologous regions C1, C2, C3, as well as regions D1 and D2. The Figure shows the amino acid sequence of C1 and D1 and marks out the occurrences of deviations therefrom in C2 and C3, and D2 respectively. Cases where a different nucleotide sequence codes for the same amino acid are indicated by "*". As will be seen there are only a very few instances where deviations in nucleotide sequence have been such as to result in expression of a different amino acid.

Example 3

(a) Purification of protein G from Streptococcus G148

The bacterium was cultured in a tryptone medium (see above) in a 12-liter fermenter. At the end of the logarithmic phase

the bacteria were harvested by centrifugation. The yield was about 100 g of bacteria (wet weight). Liberation of the cell wall protein (protein-G) from the bacteria was carried out in the manner described by Björck and Kronvall (reference above). In short, this comprises suspending the bacteria (10 % weight/volume) in 10 mM trishydroxyethyl aminomethane (Tris), pH 8.0. For digesting the bacteria we added per ml of bacteria suspension 100 microliters of 0.4 M L-cysteine (Sigma) and 80 micrograms of papain (Sigma, p-3125) dissolved in the same buffer. The mixture was incubated for 1 hr at 37 °C on a shaking table. For stopping the reaction iodoacetamide (Sigma) was added to a final concentration of 6 mM. The supernatant, about 1 liter, was removed from the mixture by centrifugation, whereupon protein G was isolated by means of chromatographic separation.

In a first step, the pH of the sample was adjusted to pH 8.0 with NaOH, and then 100 ml of DEAE Sephacel (Pharmacia AB) equilibrated in 10 mM Tris (HCl), pH 8.0, were added. The mixture was stirred for 2 hrs whereupon the gel after having been washed with the equilibrating buffer was packed onto a column (K26/40, Pharmacia AB) which was eluted with a linear gradient, 500 ml, from 0 to 0.5 M NaCl. The fractions containing protein G were detected by immunodiffusion against polyclonal IgG and were then pooled to form one sample.

In a second step, the said sample (about 220 ml) was diluted with an equal volume of PBST (30 mM Na-PO₄, 0.12 M NaCl, pH 7.2, and containing 0.05 % of Tween 20) and was mixed with 15 ml of IgG-Sepharose[®] 4B (Pharmacia AB). After 2.5 hrs of stirring the gel was washed on a glass filter and packed into a K16/20 column (Pharmacia AB). The protein was then liberated from the gel bed by isocratic elution with 0.1 M glycine (HCl), pH 2.5 (flow rate 10 ml/hr). Desalting was effected with the aid of a PD-10 column (Pharmacia AB) down to 30 mM Na-PO₄, pH 7.2.

The protein was then characterized by analytical chromatography on a Mono Q HR 5/5 column (Pharmacia AB). The chromatograms indicated that the results were very much dependent on the manner in which the papain extraction had been carried out. Two prominent peaks plus some lesser peaks of protein G activity were noted. SDS electrophoresis revealed two protein bands corresponding to MW 10,000 and MW 15,000. Table 1 sets forth the reactivity of protein G from enzyme-digested Streptococcus G148 together with the corresponding values obtained with the procedure according to Example 3(b) below.

(b) Purification and characterization of protein G produced by an E. coli strain

An E. coli strain containing the plasmid pSPG1 (see above) was employed for the production of protein G.

The bacterium was cultured in a 12-liter fermenter in a standard E. coli medium (see above). At the end of the logarithmic phase the cells were separated by centrifugation. About 560 g of bacteria (wet weight) were obtained. These were resuspended in 560 ml PBS and shredded in a mill (Dyno-Mill Type KDL, Willy A. Bachofen AG, Maschinenfabrik, Switzerland). Milling was performed with 0.1 - 0.2 mm glass beads with stirring at a rate of 3,000 rev./min. and a flow rate of 5.7 lit./hr. The supernatant, about 1,480 ml, was separated by centrifugation.

Chromatographic purification was carried out in a manner analogous to that described in Example 3(a), the principal difference being that the affinity chromatographic step was performed prior to the ion exchange step.

When the purified protein was analyzed it was found that there were two main fractions of molecular weight 30,000 and 40,000 respectively. This should be compared to the values

10,000 and 15,000 respectively obtained in the case of the papain-digested Streptococcus. However, the IgG reactivity was the same; see Table 1.

Table 2 gives a comparison of the amino acid compositions of (i) protein G from papain-extracted Streptococcus G148 (Example 3a) and (ii) protein produced by E. coli (Example 3b).

Table 3 compares protein A and protein G in respect of their affinity for various immunoglobulins. The Table sets forth the amount of each immunoglobulin required for 50 % inhibition of binding between enzyme-conjugated polyclonal rabbit IgG and immobilized protein A or protein G respectively. In view of the differences in affinity as evidenced by the results, the aforesaid protein A - protein G fusion protein is an interesting application of the present invention as shown in Example 4 (below). Correspondingly also fusion proteins are contemplated which contain active fragments of protein A and protein G - "active" in respect of immunoglobulin-binding capacity.

Example 4. Constructions of plasmid vectors encoding immunoglobulin binding activities of protein G or a fusion protein composed of protein A and protein G

In the construction work described in this Example additional manufacturers (Pharmacia AB, Sweden, and IBI (International Biotechnologies Inc., New Haven)) other than those mentioned above were used to supply for the different restriction endonucleases and the T4 DNA polymerase. The enzymes were used according to the suppliers recommendations. Between each step in the construction procedure inactivation and removal of the used enzyme (using phenol/chloroform extraction) was performed, followed by ethanol precipitation of the DNA. Finally, the DNA sample was resuspended in suitable buffer.

The E.coli strain TGI (Carter et al (1985) Nucleic Acids Res. 12: 4431-4443) was used. After transformation of the ligated samples into E.coli cells the recombinant clones were selected for ampicillin resistance.

Construction of pUG26. A subclone called pG107 containing the approx. 1,8 kb EcoRI/SalI fragment (position 0,3 to 2,1 in Fig. 1 C) from pSPG1 (Example 2) inserted between the EcoRI/SalI sites in pBR322, was used to isolate a DNA fragment coding for the immunoglobulin binding regions of protein G. As shown schematically in Fig. 4 the pG107 was digested with ThaI followed by ligation of a 8-mer oligonucleotid adapter (Pharmacia AB, Sweden, cat.no. 27-7730-01) with the recognition site for BamHI. The ligated sample was cleaved with BstNI followed by incubation with Klenow fragments and the four deoxynucleotides to fill in the BstNI restriction site thereby generating blunt ends. The latter procedure was followed by BamHI treatment and the sample was subjected to electrophoresis in an agarose gel. A DNA fragment of approx. 830 n.t. was cut out, eluted and purified. A schematic drawing of this fragment is shown in Figure 4. This fragment was ligated into pTZ18R (Pharmacia AB, Sweden, cat.no. 27-4984-01) earlier digested with XbaI followed by incubation with Klenow fragment and the four deoxynucleotides to fill in the XbaI restriction site generating a blunt end and finally digestion with BamHI. Thus, the purified BamHI/blunt end fragment, containing the immunoglobulin binding regions of protein G was ligated into pTZ18R with generated BamHI/blunt ends. After ligation the sample was transformed into freeze competent E.coli cells and a clone positive in production of protein G, called pUG26, harbouring the protein G fragment was isolated. A schematic drawing of pUG26 is shown in Figure 4.

Construction of pUG27. A derivate of pTZ18R was constructed, containing an oligonucleotide called Universal Translation Terminator (Pharmacia AB, Sweden, cat.no 27-4890-01) here

abbreviated as UTL. The construction of the pTZ18RUTL vector is also schematically shown in Figure 5. The pTZ18R was digested with PstI followed by incubation with T4 DNA polymerase to digest the sticky ends generating blunt ends to which UTL adapters were ligated. After ligation the sample was transformed into freeze competent E.coli cells and a clone harbouring one UTL-adaptor inserted into the modified PstI site was isolated and called pTZ18RUTL.

Plasmid pUG26 was digested with EcoRI/SalI and the digested sample was subjected to electrophoresis in an agarose gel and a DNA fragment of approx. 860 n.t. encoding the immunoglobulin binding regions of protein G was cut out, eluted and purified. This fragment was ligated into a EcoRI/SalI digested pTZ18RUTL vector (Figure 5).

After ligation the sample was transformed into freeze competent E.coli cells and a clone positive in production of protein G, called pUG27 was isolated. A schematic drawing of pUG27 is shown in Figure 5.

Final construction of the pAG1. To isolate a DNA fragment containing the protein A promoter and ribosomal binding sequences together with the part that encodes the signal sequence and the immunoglobulin binding regions E, D, A, B and C, a plasmid called pSPA8 (Uhlén et al 1983. Gene, 23, 369-378) was used. This plasmid was digested with BstNI followed by incubation with Klenow fragment and the four deoxynucleotides to fill in the BstNI site thereby generating blunt ends. This was followed by digestion with EcoRI. After digestion the sample was subjected to electrophoresis in an agarose gel. A DNA fragment of approx. 1200 n.t. containing the above described regions of protein A was cut out, eluted and purified. This fragment was ligated into EcoRI/SmaI digested pUG27 (Figure 5). After ligation the sample was transformed into freeze competent E.coli cells and a clone with the plasmid pAG1 was isolated harbouring

the protein A fragment (Figure 5). The pAG1 plasmid encodes a fusion molecule which is schematically drawn in Figure 6 where a more detailed description of the different junctions is included.

Construction of a plasmid vector designated to express extracellular protein G

The construction of the pE1 plasmid is schematically shown in Figure 7. The pEZZ plasmid (Nilsson et al (1986) Protein Engineering, in press) was used. The pEZZ plasmid was digested with AccI followed by religation at low concentration (1 mg/l) to delete the region between the AccI sites. The ligated sample was transformed into freeze competent E.coli cells and a clone, called pE1, was isolated, lacking the two ZZ regions.

Plasmid pUG27 was digested with BamHI/HindIII and the digested sample was subjected to electrophoresis in an agarose gel and a DNA fragment of approx. 840 n.t. containing the immunoglobulin binding regions of protein G was cut out, eluted and purified. This fragment was ligated into BamHI/HindIII digested pE1 plasmid.

Thus, after the ligation of the BamHI/HindIII fragment of pUG27 into BamHI/HindIII digested pE1, the sample was transformed into freeze competent E.coli cells and a clone positive in production of protein G, called pEG1, harbouring the protein G fragment was isolated.

Expression and purification of the pAG1 and pEG1 derived proteins

E.coli cells harbouring the pAG1 and pEG1 plasmid respectively were grown in 1 liter of E.coli liquid culture medium (see above) supplemented with ampicillin (final concentration 100 microgram/ml) over night at 37 °C. The growth

medium from the over night cultures was recovered by centrifugation and subsequently subjected to IgG affinity chromatography according to Nilsson et al 1986 (Protein Engineering, in press).

The purified proteins obtained were analysed using SDS-PAGE and the molecular weights agreed with those calculated from the deduced nucleotide sequence (approx. 31000 for the pEG1 gene product and approx. 66000 for the pAG1 gene product).

Comparative immunoglobulin binding studies

The immunoglobulin binding affinities of the pAG1 and pEG1 encoded proteins, here called protein AG and protein G respectively, were compared to commercial protein A obtained from Pharmacia AB, Sweden. The immunoglobulin binding activity of the different proteins were analyzed using a competitive ELISA technique according to Guss et al (EMBO J. 5, 1567-1575 (1986)). The different immunoglobulins were tested for their ability to inhibit the binding between alkaline phosphatase-conjugated polyclonal rabbit IgG antibodies and immobilized commercial protein A and the proteins AG and G. The results of these studies are presented in Tables 4 and 5. Note that the figures in these tables have been standardized against the binding activity to polyclonal rabbit IgG.

The figures in Table 4 show that protein A has a higher affinity than protein G derived from pEG1 to polyclonal IgG from human, guinea-pig, dog, pig and mouse. In contrast protein G derived from pEG1 shows stronger interaction with polyclonal IgG from cow, horse, goat and sheep. All three proteins interact with the same relative strength to polyclonal rat IgG and do not bind to polyclonal chicken IgG. Table 4 also presents the binding activity of the fusion

protein AG expressed from pAG1. Protein AG has affinity to all species of polyclonal IgG which bind protein A and/or protein G. Thus, as shown in Table 4 protein AG combines both protein A and G binding activity.

The affinities of proteins A, G and AG to different human myeloma immunoglobulins are presented in Table 5. Protein A shows high affinity to IgG1, IgG2 and IgG4 but not to IgG3, in contrast to protein G which shows high affinity to all IgG subclasses. Protein AG shows a high affinity to all IgG subclasses except for IgG3 to which it binds with less affinity than protein G but higher than protein A. None of the proteins A, G or AG shows any affinity to the myeloma of the IgM and IgD classes.

Conclusions

The results presented in this example show that plasmid pEG1 encodes a protein with the corresponding IgG-binding specificity as protein G encoded by pSPG1.

Furthermore, the fusion protein AG, encoded by pAG1 has in one molecule the combined IgG-binding specificity of the two separate proteins A and G.

Table 1

Immunoglobulin affinity of protein G from papain-extracted Streptococcus G148 and from E. coli containing a plasmid coding for protein G according to Examples. Assays have been carried out by way of immunodiffusion and their results are set forth as: direct precipitation, (2); ability to inhibit precipitation reaction between polyclonal bovine IgG and protein G (1); neither inhibition nor precipitation (0).

<u>Ig class</u>	<u>Streptococci</u>	<u>E. coli</u>
<u>Polyclonal IgG</u>		
human	2	2
rabbit	1	1
cow	2	2
horse	2	2
goat	2	2
guinea pig	2	2
sheep	2	2
dog	0	0
pig	2	2
rat	0	0
mouse	2	2
chicken	0	0
<u>Monoclonal murine Ig¹⁾</u>		
1 (human IgE)	1	1
1 (tpa)	2	2
2a (Ch1, C.C17)	1	1
2a (Gc, 5293.A57)	2	2
2a (Gc, R11.B6)	2	2
2a (Gc, W16.A30)	2	2
2b (Gc, C3.D1)	2	2
2b (Gc, F6.C6)	2	2
3 (Gc, C3.D14)	2	2
3 (Gc, V15.A13)	2	2

<u>Ig class</u>	<u>Streptococci</u>	<u>E. coli</u>
<u>Human myeloma proteins</u>		
IgG 1 lambda	2	2
1 kappa	2	2
2 lambda	2	2
2 kappa	2	2
3 lambda	*)	*)
3 kappa	2	2
4 lambda	2	2
4 kappa	2	2
IgM	0	0
IgA	0	*)
IgD	0	0

*) Not determined

1) As identified by names of individual monoclonals

Table 2

Comparison of amino acid contents of purified protein G (as determined in the two principal protein fractions) when derived from (i) papainextracted Streptococcus G148 and (ii) E. coli carrying a plasmid coding for protein G according to Example 3(b). Results are set forth in mole percent.

Amino acid	Streptococci G148		E. coli	
	Fract I	Fract II	Fract I	Fract II
asparagine +				
aspartic acid	13.8	12.7	7.6	8.4
threonine	18.2	21.5	15.8	18.3
serine	2.0	-	2.5	2.4
glutamine +				
glutamic acid	12.0	9.4	10.7	10.9
proline	3.2	2.1	6.5	4.8
glycine	5.9	6.6	6.0	6.1
alanine	11.3	10.7	15.9	15.5
valine	8.6	10.4	8.2	8.6
methionine	-	1.7	1.1	0.5
isoleucine	2.3	1.7	1.9	1.7
leucine	4.8	4.7	4.4	4.1
tyrosine	4.4	4.7	2.7	3.0
phenylalanine	2.9	3.0	3.0	3.0
lysine	10.6	10.7	12.7	12.1
histidine	-	-	0.4	0.2
arginine	-	-	0.6	0.4
cysteine	1)	1)	1)	1)
tryptophan	1)	1)	1)	1)

1) Not determined

Table 3

Comparison of protein A and protein G in respect of their affinity for various immunoglobulins. The Table sets forth the amount of each immunoglobulin required for 50 % inhibition of binding between enzyme-conjugated polyclonal IgG and immobilized protein A or protein G respectively. Non-reactivity is designated by "-".

Immunoglobulin	Amount (ng) required for 50 % inhibition	
	Protein G	Protein A
<u>Polyclonal IgG</u>		
human	556	263
rabbit	151	154
cow	294	3 125
horse	227	>10 000
goat	217	1 333
guinea pig	2 500	454
sheep	357	>10 000
dog	5 556	400
pig	456	179
rat	>10 000	-
mouse	1 020	333
chicken	-	-
<u>Human myeloma proteins</u>		
IgG1 lambda	250	174
1 kappa	185	111
2 lambda	208	256
2 kappa	227	256
3 kappa	345	7 404
4 lambda	210	635
4 kappa	256	250
IgM	-	-

Table 4

Relative amounts of polyclonal IgG from different species required to give a 50 % inhibition of the binding between enzyme labeled rabbit polyclonal IgG and immobilized proteins A, G or AG^{*)}.

Species	A	G	AG
Rabbit	1.0	1.0	1.0
Human	0.7	1.0	1.4
Cow	5.0	1.5	1.9
Horse	>30	0.5	7.1
Goat	3.3	3.0	2.9
Guinea-pig	0.7	13.0	1.7
Sheep	>30	1.5	11.3
Dog	0.3	6.0	0.9
Pig	0.3	3.6	1.0
Rat	>30	>30	>30
Mouse	12.0	>30	12.0
Chicken	-	-	-

*) Key to the table: The figures have been standardized to polyclonal rabbit IgG.

Table 5

Relative amounts of different human myeloma immunoglobulins required to give a 50 % inhibition of the binding between enzyme labeled rabbit polyclonal IgG and immobilized proteins A, G or AG^{*)}.

	A	G	AG
IgG1 lambda	0.2	0.5	0.4
IgG1 kappa	0.2	0.5	0.4
IgG2 lambda	1.3	2.0	1.0
IgG2 kappa	1.7	2.0	1.6
IgG3 kappa	22.0	1.0	8.0
IgG4 lambda	3.8	1.5	0.7
IgG4 kappa	0.3	1.5	0.7
IgM	-	-	-
IgD	-	-	-

^{*)} Key to the table: The figures have been standardized to polyclonal rabbit IgG.

Claims

1. Recombinant DNA molecule containing a nucleotide sequence which codes for a protein or polypeptide having the same IgG specificity as protein G from Streptococcus G148.
2. Plasmid or phage containing a nucleotide sequence which codes for a protein or polypeptide having the same IgG specificity as protein G from Streptococcus G148.
3. Microorganism containing at least one recombinant DNA molecule according to claim 1.
4. Microorganism containing at least one plasmid or phage according to claim 2.
5. Method for producing a protein or polypeptide having the same IgG specificity as protein G from Streptococcus G148, characterized in that
 - at least one recombinant DNA molecule according to claim 1 is inserted in a microorganism,
 - said microorganism is cultured in a suitable medium,
 - the protein thus formed is isolated by affinity chromatographic purification with the aid of IgG bound to an insoluble carrier.
6. Recombinant DNA molecule according to claim 1, characterized by containing one or more of the following nucleotide sequences:

ACT TAC AAA TTA ATC CTT AAT GGT AAA ACA TTG AAA GGC GAA ACA
ACT ACT GAA GCT GTT GAT GCT GCT ACT GCA GAA AAA GTC TTC AAA
CAA TAC GCT AAC GAC AAC GGT GTT GAC GGT GAA TGG ACT TAC GAC
GAT GCG ACT AAG ACC TTT ACA GTT ACT GAA

ACT TAC AAA CTT GTT ATT AAT GGT AAA ACA TTG AAA GGC GAA ACA
ACT ACT GAA GCT GTT GAT GCT GCT ACT GCA GAA AAA GTC TTC AAA
CAA TAC GCT AAC GAC AAC GGT GTT GAC GGT GAA TGG ACT TAC GAC
GAT GCG ACT AAG ACC TTT ACA GTT ACT GAA

ACT TAC AAA CTT GTT ATT AAT GGT AAA ACA TTG AAA GGC GAA ACA
ACT ACT AAA GCA GTA GAC GCA GAA ACT GCA GAA AAA GCC TTC AAA
CAA TAC GCT AAC GAC AAC GGT GTT GAT GGT GTT TGG ACT TAT GAT
GAT GCG ACT AAG ACC TTT ACG GTA ACT GAA

7. Plasmid or phage containing one or more nucleotide sequences according to claim 6.
8. Microorganism containing at least one plasmid or phage according to claim 7.
9. Recombinant DNA molecule containing a nucleotide sequence coding for protein G or an active fragment thereof fused to a gene sequence coding for protein A or an active fragment thereof.
10. Plasmid or phage containing a fused nucleotide sequence according to claim 9.
11. Microorganism containing at least one plasmid or phage according to claim 10.
12. Fusion protein or polypeptide having the combined protein A and protein G binding characteristics.
13. Fusion protein or polypeptide having the combined protein A and protein G binding characteristics produced by the use of a recombinant DNA molecule according to claim 9.

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FIG 1(a)

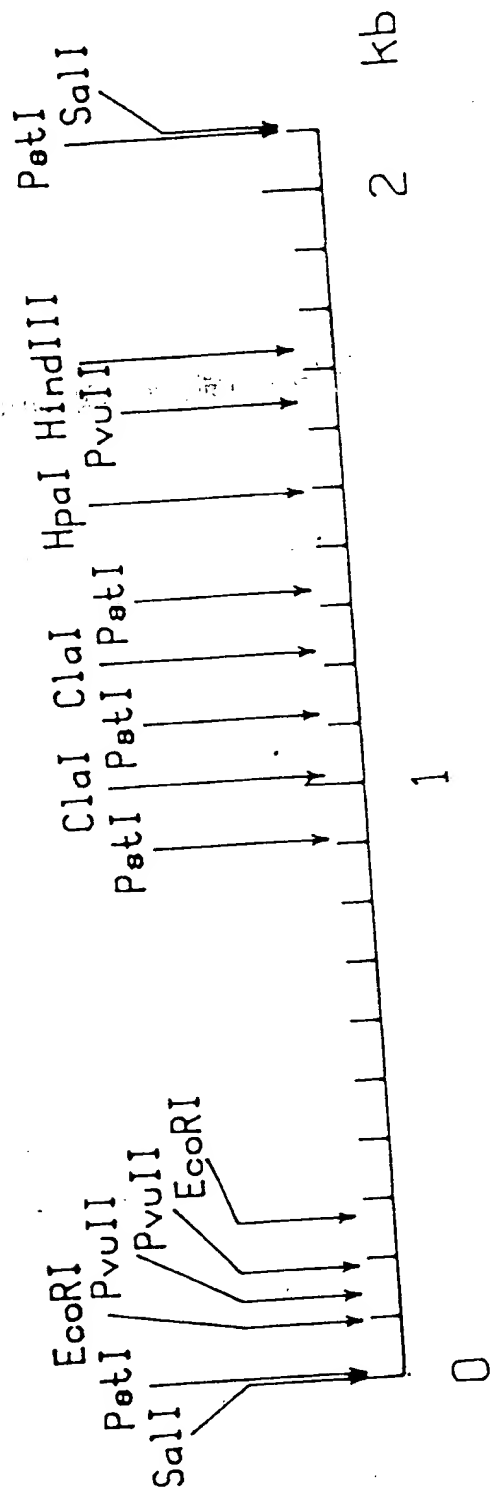
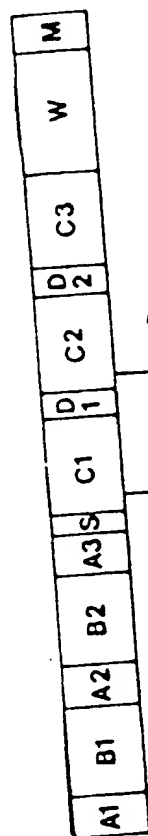


FIG 1(b)



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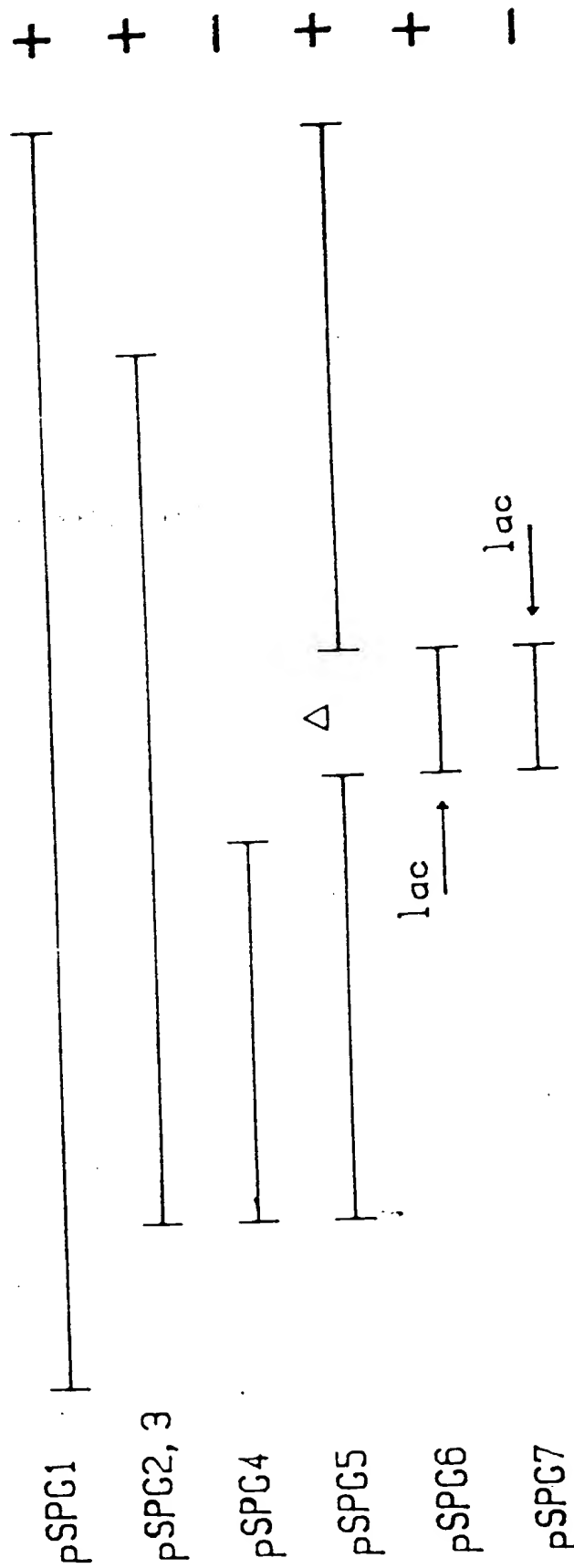


FIG 1(c)

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Fig. 2

EcoRI
 GAA TTC AAC $\xrightarrow{A1}$ AAA TAT GGA GTA AGT GAC TAT TAC AAG AAT CTA ATC 45
 Glu Phe Asn Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile

AAC AAT GCC AAA ACT GTT GAA GGC GTA AAA GAC CTT $\xrightarrow{B1}$ CAA GCA CAA 90
 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Asp Leu Gln Ala Gln

GTT GTT GAA TCA GCG AAG AAA GCG CGT ATT TCA GAA GCA ACA GAT 135
 Val Val Glu Ser Ala Lys Lys Ala Arg Ile Ser Glu Ala Thr Asp

GGC TTA TCT GAT TTC TTG AAA TCA CAA ACA CCT GCT GAA GAT ACT 180
 Gly Leu Ser Asp Phe Leu Lys Ser Gln Thr Pro Ala Glu Asp Thr

GTT AAA TCA ATT GAA TTA GCT GAA GCT AAA GTC TTA GCT AAC AGA 225
 Val Lys Ser Ile Glu Leu Ala Glu Ala Lys Val Leu Ala Asn Arg

GAA CTT GAC $\xrightarrow{A2}$ AAA TAT GGA GTA AGT GAC TAT CAC AAG AAC CTA ATC 270
 Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr His Lys Asn Leu Ile

AAC AAT GCC AAA ACT GTT GAA GGT GTA AAA GAC CTT $\xrightarrow{B2}$ CAA GCA CAA 315
 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Asp Leu Gln Ala Gln

GTT GTT GAA TCA GCG AAG AAA GCG CGT ATT TCA GAA GCA ACA GAT 360
 Val Val Glu Ser Ala Lys Lys Ala Arg Ile Ser Glu Ala Thr Asp

GGC TTA TCT GAT TTC TTG AAA TCA CAA ACA CCT GCT GAA GAT ACT 405
 Gly Leu Ser Asp Phe Leu Lys Ser Gln Thr Pro Ala Glu Asp Thr

GTT AAA TCA ATT GAA TTA GCT GAA GCT AAA GTC TTA GCT AAC AGA 450
 Val Lys Ser Ile Glu Leu Ala Glu Ala Lys Val Leu Ala Asn Arg

GAA CTT GAC $\xrightarrow{A3}$ AAA TAT GGA GTA AGT GAC TAT TAC AAG AAC CTA ATC 495
 Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile

AAC AAT GCC AAA ACT GTT GAA GGT GTA AAA GCA CTG \xrightarrow{S} ATA GAT GAA 540
 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu

ATT TTA GCT GCA TTA CCT AAG ACT GAC $\xrightarrow{C1}$ ACT TAC AAA TTA ATC CTT 585
 Ile Leu Ala Ala Leu Pro Lys Thr Asp Thr Tyr Lys Leu Ile Leu

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Fig. 2 (cont.)

AAT GGT AAA ACA TTG AAA GGC GAA ACA ACT ACT GAA GCT GTT GAT 630
 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp

PstI
 GCT GCT ACT GCA GAA AAA GTC TTC AAA CAA TAC GCT AAC GAC AAC 675
 Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn

GGT GTT GAC GGT GAA TGG ACT TAC GAC GAT GCG ACT AAG ACC TTT 720
 Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe

ACA GTT ACT GAA AAA CCA GAA GTG ATC GAT GCG TCT GAA TTA ACA 765
 Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr

CCA GCC GTG ACA ACT TAC AAA CTT GTT ATT AAT GGT AAA ACA TTG 810
 Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu

PstI
 AAA GGC GAA ACA ACT ACT GAA GCT GTT GAT GCT GCT ACT GCA GAA 855
 Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu

AAA GTC TTC AAA CAA TAC GCT AAC GAC AAC GGT GTT GAC GGT GAA 900
 Lys Val Phe Lys Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu

TGG ACT TAC GAC GAT GCG ACT AAG ACC TTT ACA GTT ACT GAA AAA 945
 Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys

CCA GAA GTG ATC GAT GCG TCT GAA TTA ACA CCA GCC GTG ACA ACT 990
 Pro Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr

TAC AAA CTT GTT ATT AAT GGT AAA ACA TTG AAA GGC GAA ACA ACT 1035
 Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr

PstI
 ACT AAA GCA GTA GAC GCA GAA ACT GCA GAA AAA GCC TTC AAA CAA 1080
 Thr Lys Ala Val Asp Ala Glu Thr Ala Glu Lys Ala Phe Lys Gln

TAC GCT AAC GAC AAC GGT GTT GAT GGT GTT TGG ACT TAT GAT GAT 1125
 Tyr Ala Asn Asp Asn Gly Val Asp Gly Val Trp Thr Tyr Asp Asp

GCG ACT AAG ACC TTT ACG GTA ACT GAA ATG GTT ACA GAG GTT CCT 1170
 Ala Thr Lys Thr Phe Thr Val Thr Glu Met Val Thr Glu Val Pro

GGT GAT GCA CCA ACT GAA CCA GAA AAA CCA GAA GCA AGT ATC CCT 1215
 Gly Asp Ala Pro Thr Glu Pro Glu Lys Pro Glu Ala Ser Ile Pro

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Fig. 2 (cont)

HpaI

TTT GTT CCG TTA ACT CCT GCA ACT CCA ATT GCT AAA GAT GAC GCT 1260
 Leu Val Pro Leu Thr Pro Ala Thr Pro Ile Ala Lys Asp Asp Ala

AAG AAA GAC GAT ACT AAG AAA GAA GAT GCT AAA AAA CCA GAA GCT 1305
 Lys Lys Asp Asp Thr Lys Lys Glu Asp Ala Lys Lys Pro Glu Ala

AAG AAA GAA GAC GCT AAG AAA GCT GAA ACT CTT CCT ACA ACT GGT 1350
 Lys Lys Glu Asp Ala Lys Lys Ala Glu Thr Leu Pro Thr Thr Gly

GAA GGC AGC AAC CCA ^MTTC TTC ACA GCA ^{PvuII}GCT GCG CTT GCA GTA ATG 1395
 Glu Gly Ser Asn Pro Phe Phe Thr Ala Ala Ala Leu Ala Val Met

GCT GGT GCG GGT GCT TTG GCG GTC GCT TCA AAA CGT AAA GAA GAC 1440
 Ala Gly Ala Gly Ala Leu Ala Val Ala Ser Lys Arg Lys Glu Asp

HindIII

TAA TTGTCATTATTTTGGACAAAAGCTT

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Fig 3

	ACT	TAC	AAA	TTA	ATC	CTT	AAT	GGT	AAA	ACA	TTG	AAA	GGC	GAA	ACA	ACT
C1	Thr	Tyr	Lys	Leu	Ile	Leu	Asn	Gly	Lys	Thr	Leu	Lys	Gly	Glu	Thr	Thr
C2	-	-	-	*	Val	Ile	-	-	-	-	-	-	-	-	-	-
C3	-	-	-	*	Val	Ile	-	-	-	-	-	-	-	-	-	-

	ACT	GAA	GCT	GTT	GAT	GCT	GCT	ACT	GCA	GAA	AAA	GTC	TTC	AAA	CAA	TAC
C1	Thr	Glu	Ala	Val	Asp	Ala	Ala	Thr	Ala	Glu	Lys	Val	Phe	Lys	Gln	Tyr
C2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C3	-	Lys	*	*	*	*	Glu	-	-	-	-	Ala	-	-	-	-

	GCT	AAC	GAC	AAC	GGT	GTT	GAC	GGT	GAA	TGG	ACT	TAC	GAC	GAT	GCG	ACT
C1	Ala	Asn	Asp	Asn	Gly	Val	Asp	Gly	Glu	Trp	Thr	Tyr	Asp	Asp	Ala	Thr
C2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C3	-	-	-	-	-	-	-	-	Val	-	-	*	*	-	-	-

	AAG	ACC	TTT	ACA	GTT	ACT	GAA		AAA	CCA	GAA	GTG	ATC	GAT	GCG
C1	Lys	Thr	Phe	Thr	Val	Thr	Glu	D1	Lys	Pro	Glu	Val	Ile	Asp	Ala
C2	-	-	-	-	-	-	-	D2	-	-	-	-	-	-	-
C3	-	-	-	*	*	-	-								

	TCT	GAA	TTA	ACA	CCA	GCC	GTG	ACA
D1	Ser	Glu	Leu	Thr	Pro	Ala	Val	Thr
D2	-	-	-	-	-	-	-	-

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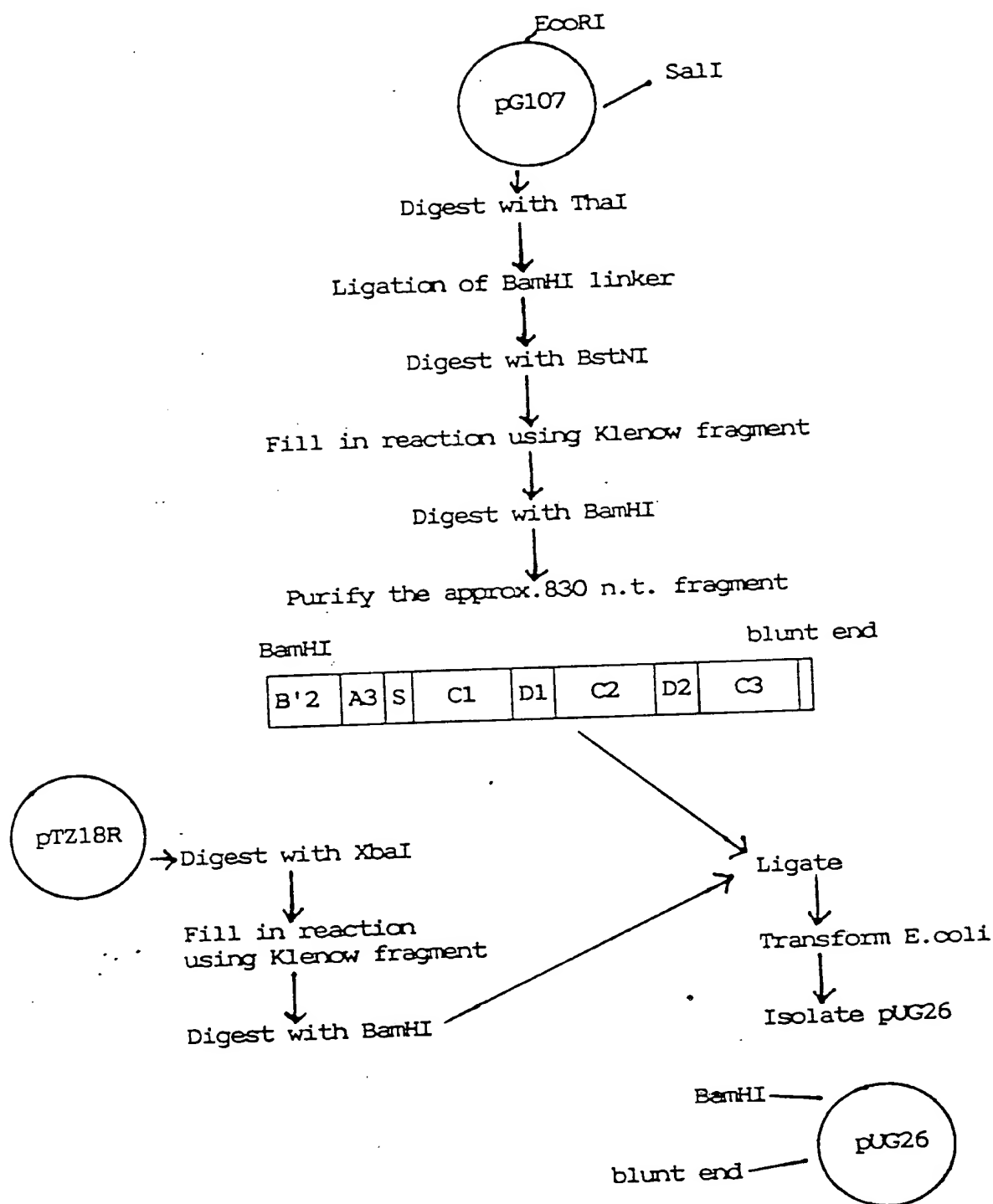


Fig 4.

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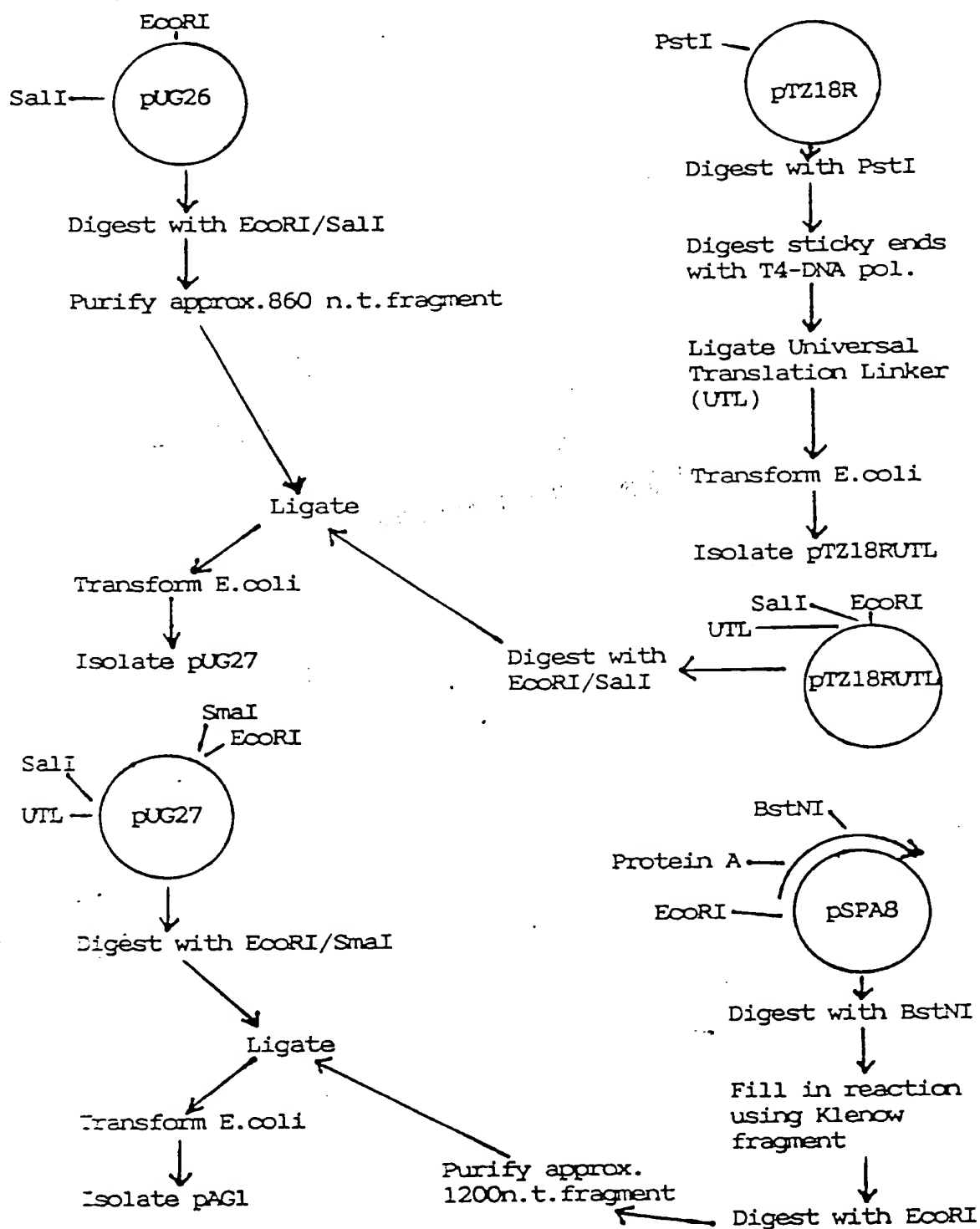
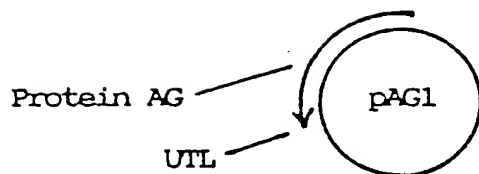


Fig.5

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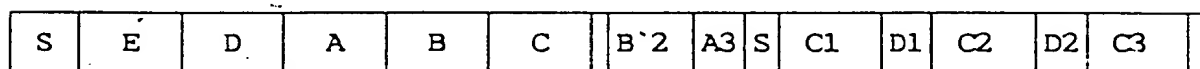
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The immunoglobulin binding fusionprotein protein AG encoded by pAG1

NH₂ terminal part
originating from protein A

COOH terminal part
originating from protein G



*** OCT GGG GAT OCG CGT ***
Pro Gly Asp Pro Arg
protein A -----< >----- protein G

*** OCT CTA GAG TCG ACC GCT TAA
Pro Leu Glu Ser Thr Ala Stop
protein G -----<

Fig. 6

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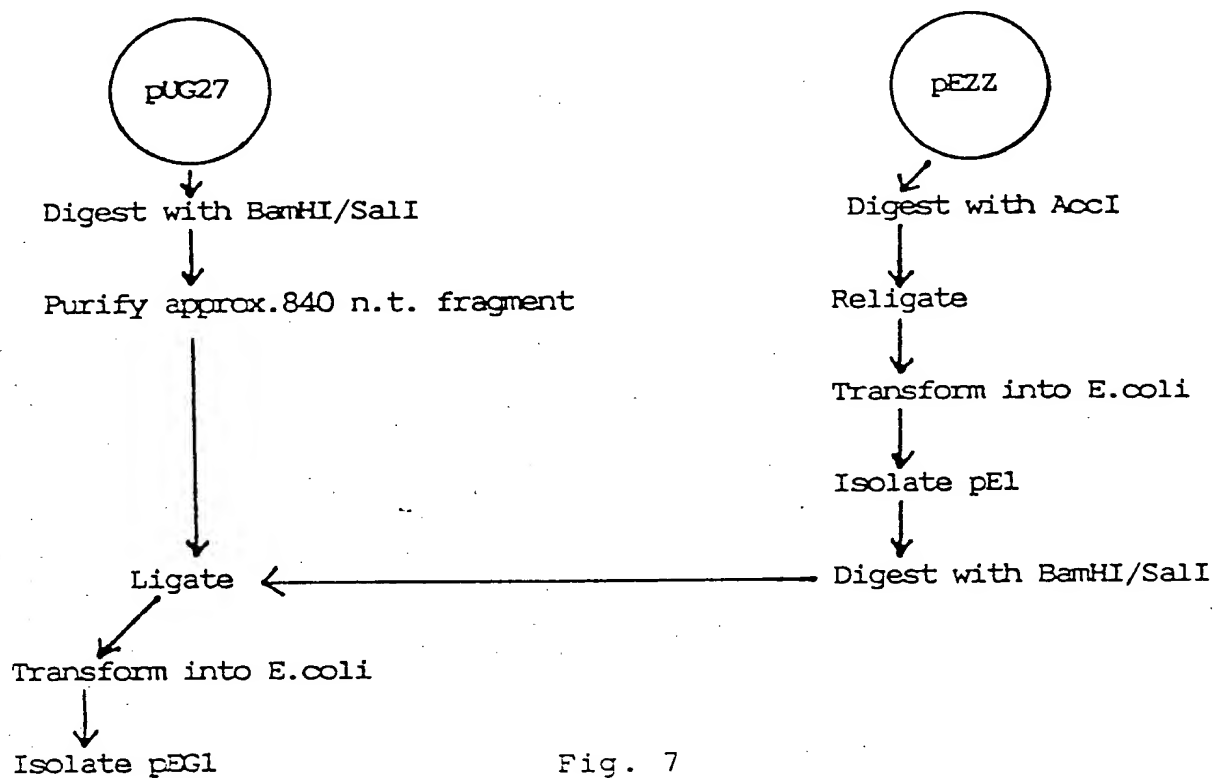


Fig. 7

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INTERNATIONAL SEARCH REPORT

International Application No. PCT/SE87/00145

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) ⁶ According to International Patent Classification (IPC) or to both National Classification and IPC ⁴ <div style="text-align: center; margin-top: 10px;">C 12 N 15/00</div>																	
II. FIELDS SEARCHED <div style="text-align: center; margin-top: 10px;">Minimum Documentation Searched ⁷</div> <table border="1" style="width: 100%; border-collapse: collapse; margin-top: 5px;"> <tr> <th style="width: 20%;">Classification System</th> <th style="width: 80%;">Classification Symbols</th> </tr> <tr> <td style="padding: 5px;">IPC 4 US C1</td> <td style="padding: 5px;">C 12 N 15/00; C 12 P 21/00 435: 68, 70, 172</td> </tr> </table> <div style="text-align: center; margin-top: 10px;">Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched ⁸</div> <div style="text-align: center; margin-top: 10px;">SE, NO, DK, FI classes as above Data base search: CA, WPI, WPIL, Telegen, Biosis</div>			Classification System	Classification Symbols	IPC 4 US C1	C 12 N 15/00; C 12 P 21/00 435: 68, 70, 172											
Classification System	Classification Symbols																
IPC 4 US C1	C 12 N 15/00; C 12 P 21/00 435: 68, 70, 172																
III. DOCUMENTS CONSIDERED TO BE RELEVANT ⁹ <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="width: 10%;">Category ¹⁰</th> <th style="width: 60%;">Citation of Document, ¹¹ with Indication, where appropriate, of the relevant passages ¹²</th> <th style="width: 30%;">Relevant to Claim No. ¹³</th> </tr> </thead> <tbody> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">P</td> <td style="padding: 5px;">SE, A, 8502162-4 (EXCORIM) 4 November 1986</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-13</td> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">EP, A1, 0 124 374 (GENEX CORPORATION) 7 November 1974 & JP, 59205996 US, 4617266</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-13</td> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">SE, A, 8303578- 2 (GAMBRO) 23 December 1984</td> <td style="text-align: center; vertical-align: top; padding: 5px;">1-13</td> </tr> <tr> <td style="text-align: center; vertical-align: top; padding: 5px;">Y</td> <td style="padding: 5px;">WO, A1, 84/03103 (PHARMACIA AB) 16 August 1984 & SE, 830C693 EP, 0135532 JP, 60500480</td> <td style="text-align: center; vertical-align: top; padding: 5px;">9-13</td> </tr> </tbody> </table>			Category ¹⁰	Citation of Document, ¹¹ with Indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³	P	SE, A, 8502162-4 (EXCORIM) 4 November 1986	1-13	Y	EP, A1, 0 124 374 (GENEX CORPORATION) 7 November 1974 & JP, 59205996 US, 4617266	1-13	Y	SE, A, 8303578- 2 (GAMBRO) 23 December 1984	1-13	Y	WO, A1, 84/03103 (PHARMACIA AB) 16 August 1984 & SE, 830C693 EP, 0135532 JP, 60500480	9-13
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<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p>¹⁰ Special categories of cited documents: ¹⁰</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&" document member of the same patent family</p> </div> </div>																	
IV. CERTIFICATION <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 50%; padding: 5px;">Date of the Actual Completion of the International Search</td> <td style="width: 50%; padding: 5px;">Date of Mailing of this International Search Report</td> </tr> <tr> <td style="text-align: center; padding: 5px;">1987-05-21</td> <td style="text-align: center; padding: 5px;">1987 -06- 0 3</td> </tr> <tr> <td style="padding: 5px;">International Searching Authority Swedish Patent Office</td> <td style="padding: 5px;">Signature of Authorized Officer <i>Yvonne Siösteen</i> Yvonne Siösteen</td> </tr> </table>			Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report	1987-05-21	1987 -06- 0 3	International Searching Authority Swedish Patent Office	Signature of Authorized Officer <i>Yvonne Siösteen</i> Yvonne Siösteen									
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